



IFWP

RAW SEQUENCE LISTING

DATE: 07/10/2006

PATENT APPLICATION: US/10/584,810

TIME: 10:24:35

Input Set : A:\21471 SEQ LSTG 6 16 06.TXT

Output Set: N:\CRF4\07102006\J584810.raw

4 <110> APPLICANT: Merck & Co., Inc.
 6 <120> TITLE OF INVENTION: HCV RNA-DEPENDENT RNA POLYMERASE
 9 <130> FILE REFERENCE: 21471 PCT
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/584,810
 C--> 11 <141> CURRENT FILING DATE: 2006-06-28
 11 <150> PRIOR APPLICATION NUMBER: 60/535,708
 12 <151> PRIOR FILING DATE: 2004-01-09
 14 <160> NUMBER OF SEQ ID NOS: 28
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 571
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Artificial Sequence
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: modified HCV NS5B
 26 <400> SEQUENCE: 1
 27 Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ser
 28 1 5 10 15
 29 Pro Glu Glu Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Leu
 30 20 25 30
 31 Arg Tyr His Asn Lys Val Tyr Cys Thr Thr Thr Lys Ser Ala Ser Leu
 32 35 40 45
 33 Arg Ala Lys Lys Val Thr Phe Asp Arg Met Gln Val Leu Asp Ser Tyr
 34 50 55 60
 35 Tyr Asp Ser Val Leu Lys Asp Ile Lys Leu Ala Ala Ser Lys Val Thr
 36 65 70 75 80
 37 Ala Arg Leu Leu Thr Met Glu Glu Ala Cys Gln Leu Thr Pro Pro His
 38 85 90 95
 39 Ser Ala Arg Ser Lys Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu
 40 100 105 110
 41 Ser Gly Arg Ala Val Asn His Ile Lys Ser Val Trp Lys Asp Leu Leu
 42 115 120 125
 43 Glu Asp Ser Glu Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
 44 130 135 140
 45 Val Phe Cys Val Asp Pro Thr Lys Gly Gly Lys Lys Ala Ala Arg Leu
 46 145 150 155 160
 47 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
 48 165 170 175
 49 Tyr Asp Ile Thr Gln Lys Leu Pro Gln Ala Val Met Gly Ala Ser Tyr
 50 180 185 190
 51 Gly Phe Gln Tyr Ser Pro Ala Gln Arg Val Glu Phe Leu Leu Lys Ala
 52 195 200 205
 53 Trp Ala Glu Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys

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```

54      210      215      220
55 Phe Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile
56 225      230      235      240
57 Tyr Arg Ala Cys Ser Leu Pro Glu Glu Ala His Thr Ala Ile His Ser
58      245      250      255
59 Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly
60      260      265      270
61 Gln Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
62      275      280      285
63 Ser Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys
64      290      295      300
65 Lys Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp
66 305      310      315      320
67 Leu Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn
68      325      330      335
69 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
70      340      345      350
71 Asp Pro Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
72      355      360      365
73 Ser Asn Val Ser Val Ala Leu Gly Pro Gln Gly Arg Arg Arg Tyr Tyr
74      370      375      380
75 Leu Thr Arg Asp Pro Thr Thr Pro Ile Ala Arg Ala Ala Trp Glu Thr
76 385      390      395      400
77 Val Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr
78      405      410      415
79 Ala Pro Thr Ile Trp Ala Arg Met Val Leu Met Thr His Phe Phe Ser
80      420      425      430
81 Ile Leu Met Ala Gln Asp Thr Leu Asp Gln Asn Leu Asn Phe Glu Met
82      435      440      445
83 Tyr Gly Ala Val Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
84      450      455      460
85 Glu Arg Leu His Gly Leu Asp Ala Phe Ser Leu His Thr Tyr Thr Pro
86 465      470      475      480
87 His Glu Leu Thr Arg Val Ala Ser Ala Leu Arg Lys Leu Gly Ala Pro
88      485      490      495
89 Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
90      500      505      510
91 Ile Ser Arg Gly Gly Arg Ala Ala Val Cys Gly Arg Tyr Leu Phe Asn
92      515      520      525
93 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Arg
94      530      535      540
95 Leu Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
96 545      550      555      560
97 Ile Tyr His Ser Val Ser Arg Ala Arg Pro Arg
98      565      570

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101 <210> SEQ ID NO: 2

102 <211> LENGTH: 571

103 <212> TYPE: PRT

104 <213> ORGANISM: Artificial Sequence

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106 <220> FEATURE:

107 <223> OTHER INFORMATION: modified HCV NS5B

109 <400> SEQUENCE: 2

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110 Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly
111 1 5 10 15
112 Pro Glu Glu Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Met
113 20 25 30
114 Arg Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu
115 35 40 45
116 Arg Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His
117 50 55 60
118 Tyr Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser
119 65 70 75 80
120 Ala Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His
121 85 90 95
122 Ser Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu
123 100 105 110
124 Ser Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu
125 115 120 125
126 Glu Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu
127 130 135 140
128 Val Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu
129 145 150 155 160
130 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
131 165 170 175
132 Tyr Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr
133 180 185 190
134 Gly Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala
135 195 200 205
136 Trp Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
137 210 215 220
138 Phe Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile
139 225 230 235 240
140 Tyr Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser
141 245 250 255
142 Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly
143 260 265 270
144 Gln Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr
145 275 280 285
146 Ser Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys
147 290 295 300
148 Lys Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp
149 305 310 315 320
150 Leu Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn
151 325 330 335
152 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
153 340 345 350
154 Asp Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
155 355 360 365

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```

156 Ser Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Arg Tyr Phe
157      370      375      380
158 Leu Thr Arg Asp Pro Thr Thr Pro Ile Thr Arg Ala Ala Trp Glu Thr
159 385      390      395      400
160 Val Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr
161      405      410      415
162 Ala Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser
163      420      425      430
164 Ile Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met
165      435      440      445
166 Tyr Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile
167      450      455      460
168 Glu Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro
169 465      470      475      480
170 His Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro
171      485      490      495
172 Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
173      500      505      510
174 Ile Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn
175      515      520      525
176 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser
177      530      535      540
178 Arg Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
179 545      550      555      560
180 Ile Tyr His Ser Val Ser His Ala Arg Pro Arg
181      565      570
184 <210> SEQ ID NO: 3
185 <211> LENGTH: 571
186 <212> TYPE: PRT
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: modified HCV NS5B
192 <400> SEQUENCE: 3
193 Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ser
194 1      5      10      15
195 Ala Glu Glu Glu Lys Leu Pro Ile Ser Pro Leu Ser Asn Ser Leu Leu
196      20      25      30
197 Arg His His Asn Leu Val Tyr Ser Thr Ser Ser Arg Ser Ala Ser Gln
198      35      40      45
199 Arg Gln Arg Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
200      50      55      60
201 Tyr Lys Thr Ala Leu Lys Glu Val Lys Glu Arg Ala Ser Arg Val Lys
202 65      70      75      80
203 Ala Arg Met Leu Thr Ile Glu Glu Ala Cys Ala Leu Val Pro Pro His
204      85      90      95
205 Ser Ala Arg Ser Lys Phe Gly Tyr Ser Ala Lys Asp Val Arg Ser Leu
206      100      105      110
207 Ser Ser Arg Ala Ile Asp Gln Ile Arg Ser Val Trp Glu Asp Leu Leu
208      115      120      125

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```

209 Glu Asp Thr Thr Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
210      130      135      140
211 Val Phe Cys Val Asp Pro Ala Lys Gly Gly Arg Lys Pro Ala Arg Leu
212 145      150      155      160
213 Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Arg Ala Leu
214      165      170      175
215 Tyr Asp Val Ile Gln Lys Leu Ser Ile Glu Thr Met Gly Ser Ala Tyr
216      180      185      190
217 Gly Phe Gln Tyr Ser Pro Gln Gln Arg Val Glu Arg Leu Leu Lys Met
218      195      200      205
219 Trp Thr Ser Lys Lys Thr Pro Leu Gly Phe Ser Tyr Asp Thr Arg Cys
220      210      215      220
221 Phe Asp Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile
222 225      230      235      240
223 Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser
224      245      250      255
225 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
226      260      265      270
227 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
228      275      280      285
229 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
230      290      295      300
231 Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
232 305      310      315      320
233 Leu Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala
234      325      330      335
235 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
236      340      345      350
237 Asp Ala Pro Gln Pro Thr Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
238      355      360      365
239 Ser Asn Val Ser Val Ala Arg Asp Asp Lys Gly Arg Arg Tyr Tyr Tyr
240      370      375      380
241 Leu Thr Arg Asp Ala Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
242 385      390      395      400
243 Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr
244      405      410      415
245 Ala Pro Thr Ile Trp Val Arg Met Val Met Met Thr His Phe Phe Ser
246      420      425      430
247 Ile Leu Gln Ser Gln Glu Ile Leu Asp Arg Pro Leu Asp Phe Glu Met
248      435      440      445
249 Tyr Gly Ala Thr Tyr Ser Val Thr Pro Leu Asp Leu Pro Ala Ile Ile
250      450      455      460
251 Glu Arg Leu His Gly Leu Ser Ala Phe Thr Leu His Ser Tyr Ser Pro
252 465      470      475      480
253 Val Glu Leu Asn Arg Val Ala Gly Thr Leu Arg Lys Leu Gly Cys Pro
254      485      490      495
255 Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
256      500      505      510
257 Ile Ala Gln Gly Gly Lys Ala Lys Ile Cys Gly Leu Tyr Leu Phe Asn

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VERIFICATION SUMMARY

DATE: 07/10/2006

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Input Set : A:\21471 SEQ LSTG 6 16 06.TXT

Output Set: N:\CRF4\07102006\J584810.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date